

---

**Comprehensive microRNA profiling reveals a unique human embryonic stem cell signature dominated by a single seed sequence.**

**Journal:** Stem Cells

**Publication Year:** 2008

**Authors:** Louise C Laurent, Jing Chen, Igor Ulitsky, Franz-Josef Mueller, Christina Lu, Ron Shamir, Jian-Bing Fan, Jeanne F Loring

**PubMed link:** 18403753

**Funding Grants:** Interdisciplinary Stem Cell Training Program at UCSD

**Public Summary:**

**Scientific Abstract:**

Embryonic stem cells are unique among cultured cells in their ability to self-renew and differentiate into a wide diversity of cell types, suggesting that a specific molecular control network underlies these features. Human embryonic stem cells (hESCs) are known to have distinct mRNA expression, global DNA methylation, and chromatin profiles, but the involvement of high-level regulators, such as microRNAs (miRNA), in the hESC-specific molecular network is poorly understood. We report that global miRNA expression profiling of hESCs and a variety of stem cell and differentiated cell types using a novel microarray platform revealed a unique set of miRNAs differentially regulated in hESCs, including numerous miRNAs not previously linked to hESCs. These hESC-associated miRNAs were more likely to be located in large genomic clusters, and less likely to be located in introns of coding genes. hESCs had higher expression of oncogenic miRNAs and lower expression of tumor suppressor miRNAs than the other cell types. Many miRNAs upregulated in hESCs share a common consensus seed sequence, suggesting that there is cooperative regulation of a critical set of target miRNAs. We propose that miRNAs are coordinately controlled in hESCs, and are key regulators of pluripotency and differentiation. Disclosure of potential conflicts of interest is found at the end of this article.

---

**Source URL:** <https://www.cirm.ca.gov/about-cirm/publications/comprehensive-microrna-profiling-reveals-unique-human-embryonic-stem-cell>